



Draft Genome Sequences of Spacecraft-Associated Microbes Isolated from Six NASA Missions

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ABSTRACT Whole-genome sequencing can be used to better understand and assess the functional abilities of microorganisms isolated from spacecraft hardware and associated surfaces for planetary protection (PP) purposes. We sequenced 191 isolates from 6 spaceflight missions with PP requirements and identified them using Illumina-based sequencing methods and matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry.

The microbial archive at the Jet Propulsion Laboratory (JPL) contains over 8,000 bacterial strains previously isolated from missions with planetary protection (PP) requirements. The Genome Encyclopedia of Spacecraft Associated Microbes (GESAM) project has set out to perform a high-throughput identification of bacterial isolates spanning 6 past spaceflight missions from 1975 to 2012 (Viking, Mars Pathfinder, Mars Odyssey, Mars Exploration Rover [MER], Phoenix, and Mars Science Laboratory [MSL]). These PP-sensitive missions must minimize biological contamination on hardware surfaces to preserve the scientific integrity of mission objectives. The NASA standard assay was used throughout the mission timelines to assess hardware cleanliness. The assay involved heat-shocking samples at 80°C for 15 min, plating them on Trypticase soy agar (TSA), and incubating them for 72 h at 32°C (1). The resulting colonies were subcultured and stored long term in the JPL microbial archive following previously established procedures (1). In 2019, 1,418 stored isolates were revived from three replicate glycerol stocks and incubated for 72 h on TSA at 32°C. Of those, 1,249 strains displayed growth within 72 h and were inspected for colony morphology and visual purity across multiple stocks.

These 1,249 pure strains were screened using matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) and 16S rRNA sequencing for rapid, comprehensive identification filtering for the most abundant and potentially novel isolates. MALDI-TOF MS is a rapid and systematic identification method that uses the main spectrum profiles of isolates, composed of at least 10 spectra each. If MALDI-TOF MS did not match the isolate to a custom in-house MALDI-TOF MS database (2) (with at least 3 replicates with a log score of >2.2 for species level identification and >2.0 for genus level, for stringency and quality control), DNA was extracted, and the 16S rRNA gene was sequenced. DNA extraction was performed using the Maxwell rapid sample concentrator (RSC) automated DNA extraction instrument and the Maxwell RSC blood DNA extraction kit (Promega, USA). DNA was eluted in 10 mM Tris-HCl (pH 8.0) and quantified using the Quant-iT double-stranded DNA (dsDNA) high-sensitivity (HS) kit and Qubit fluorometer (Thermo Fisher, USA). The DNA was sent to MicrobesNG (UK) for library preparation and sequencing. 16S amplicon libraries were prepared using the Nextera XT library prep kit (Illumina, USA) using the manufacturer's protocol with the following modifications: (i) the input DNA was increased 2-fold, and (ii) the PCR elongation time was increased to

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TABLE 1 Genome statistics for the 191 draft genomes isolated from 6 NASA mission spacecraft and associated surfaces^a

Strain name	Taxonomic identification	Date of isolation (yr/ mo/day)	GenBank accession no.	SRA accession no. for Illumina reads	G+C content (%)	No. of contigs	No. of Illumina reads	Genome assembly N ₅₀ (bp)	No. of protein-coding genes	No. of complete rRNAs (5S, 16S, 23S)	No. of genome size (bp)	Genome coverage (×)
41.1	<i>Brevibacillus invocatus</i>	2008-05-14	JAMATE00000000000	SRX16346898	48.77	195	2,047,596	110,673	4,771	5,0,0	4,876,904	456
68.1	<i>Bacillus safensis</i>	2008-10-03	JAMATB00000000000	SRX16346899	41.77	52	870,943	953,608	3,699	5,1,0	3,696,265	150
154.2	<i>Bacillus subtilis</i>	2008-08-08	JAMATC00000000000	SRX16346910	44.73	427	1,356,939	1,071,018	4,462	8,1,0	4,283,513	348
183.1	<i>Caldibacillus thermoamylolyticus</i>	2008-08-08	JAMATD00000000000	SRX16346921	37.46	156	1,698,559	107,952	3,529	8,0,0	3,833,088	492
197.1	<i>Staphylococcus warneri</i>	2008-12-12	JAMATE00000000000	SRX16346932	32.57	57	909,941	451,487	2,440	5,1,0	2,575,646	396
251.1	<i>Bacillus altitudinis</i>	2009-01-05	JAMATH00000000000	SRX16346933	41.33	46	1,245,875	844,862	3,718	5,1,1	3,714,328	371
128.1.2	<i>Mesobacillus maritimus</i>	2009-01-15	JAMBNU00000000000	SRX16346934	38.92	186	1,591,579	205,680	4,914	21,0,0	5,283,993	333
206.2.2	<i>Bacillus amylolyticus</i>	2008-12-27	JAMATF00000000000	SRX16346935	46.24	69	1,223,409	875,626	3,703	8,0,0	3,759,069	361
214.1.1	<i>Alkalihalobacillus oceanii</i>	2009-01-03	JAMBOL00000000000	SRX16346936	46.43	124	1,484,379	165,889	4,264	9,0,0	4,474,054	367
236.1.1	<i>Bacillus altitudinis</i>	2009-01-03	JAMATG00000000000	SRX16346937	41.42	75	1,134,683	844,862	3,754	5,1,0	3,727,933	338
258.1A	<i>Lederbergia lenta</i>	2009-01-05	JAMATI00000000000	SRX16346900	36.47	47	1,268,550	1,157,153	4,411	9,0,0	4,617,171	307
AMY 1.1.1	<i>Bhargavaea ginsengii</i>	2009-01-05	JAMATJ00000000000	SRX16346901	53.68	108	614,536	106,446	3,125	7,0,0	3,187,319	207
AMY 11.1.2	<i>Staphylococcus warneri</i>	2007-05-31	JAMATN00000000000	SRX16346902	32.74	48	814,382	550,861	2,372	4,0,0	2,485,735	357
AMY 13.1.2	<i>Piestia megalterium</i>	2007-06-01	JAMATO00000000000	SRX16346903	37.65	105	1,886,191	2,128,716	5,721	16,0,0	5,722,597	368
AMY 15.2	<i>Cytobacillus sp.</i>	2007-06-01	JAMATP00000000000	SRX16346904	41.25	174	1,663,153	155,819	5,147	8,0,1	5,257,607	350
AMY 19.1.2	<i>Fictibacillus phosphorivorans</i>	2007-06-05	JAMBOR00000000000	SRX16346905	39.99	101	1,272,624	131,198	3,643	5,0,0	3,689,124	386
AMY 19.1.2 vial 1	<i>Fictibacillus phosphorivorans</i>	2007-06-05	JAMBOD00000000000	SRX16346906	40.02	559	1,365,050	131,198	3,675	5,0,0	3,903,370	390
AMY 2.1.4	<i>Staphylococcus equorum</i>	2007-08-31	JAMATK00000000000	SRX16346907	32.96	40	604,049	1,097,483	2,726	7,1,0	2,876,286	229
AMY 24.1.1	<i>Bacillus safensis</i>	2007-06-01	JAMATQ00000000000	SRX16346908	41.37	63	982,797	652,330	4,022	4,0,1	3,934,836	276
AMY 31.1.2	<i>Bacillus pumilus</i>	2007-06-01	JAMATR00000000000	SRX16346909	41.67	34	830,701	1,900,424	3,654	5,1,0	3,673,368	251
AMY 5.1.1	<i>Cytobacillus firmus</i>	2007-05-11	JAMATU00000000000	SRX16346911	41.66	67	874,120	446,334	3,768	5,0,1	3,777,130	257
AMY 52	<i>Oceanobacillus luteolus</i>	2007-05-11	JAMBON00000000000	SRX16346912	41.17	212	1,049,930	66,879	4,822	9,0,0	4,922,695	236
AMY 6.1.1	<i>Bacillus licheniformis</i>	2007-05-20	JAMATV00000000000	SRX16346913	38.89	207	1,216,340	89,594	3,891	8,0,0	4,009,121	338
AMY 7.1	<i>Piestia flexa</i>	2007-05-19	JAMATW00000000000	SRX16346914	46.29	62	1,376,333	387,437	4,063	7,0,1	4,098,880	368
CFPSW 5.3	<i>Cytobacillus oceanisediminis</i>	2008-04-10	JAMATT00000000000	SRX16346915	37.96	255	2,202,843	62,929	3,852	10,1,0	3,867,371	637
				SRX16346916	40.94	106	1,436,564	289,172	5,683	10,0,0	5,770,654	274
FAIRING 10M-2.2	<i>Bacillus cytotoxicus</i>	2004-04-21	JAMBOP00000000000	SRX16346917	36.22	159	1,793,913	119,518	4,382	8,1,0	4,644,912	417
FAIRING 12A-4	<i>Heyndrickxia oleorolia</i>	2007-01-23	JAMATV00000000000	SRX16346918	34.88	95	2,158,617	634,364	5,028	12,0,0	5,270,304	448
FAIRING 19B-1.2	<i>Staphylococcus warneri</i>	2007-01-27	JAMATX00000000000	SRX16346919	32.28	60	913,332	426,680	2,345	6,1,1	2,487,207	410
FAIRING 3B-1.2	<i>Bacillus velezensis</i>	2013-08-19	JAMATU00000000000	SRX16346920	46.18	438	769,918	81,1,981	4,235	7,0,1	4,212,269	204
FAIRING 4G-1.1	<i>Staphylococcus epidermidis</i>	2013-08-20	JAMATV00000000000	SRX16346922	31.94	74	1,100,052	167,417	2,385	6,0,1	2,585,673	474
FAIRING W8B-1	<i>Stenotrophomonas maltophilia</i>	2013-08-19	JAMATY00000000000	SRX16346923	66.54	73	535,590	175,432	4,439	3,0,1	4,898,338	118
KSC 114	<i>Bacillus safensis</i>	2013-10	JAMATZ00000000000	SRX16346924	41.3	33	702,844	483,649	3,738	5,0,1	3,712,377	206
KSC 155	<i>Bacillus subtilis</i>	2013-10	JAMAUA00000000000	SRX16346925	41	82	1,190,920	672,012	3,809	5,1,0	3,813,861	344
KSC 283	<i>Piestia megalterium</i>	2013-10	JAMAUB00000000000	SRX16346926	38.25	146	1,524,780	497,735	5,282	14,1,0	5,197,219	322

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TABLE 1 (Continued)

Strain name	Taxonomic identification	Date of isolation (yr/mo/day)	GenBank accession no.	SRA accession no. for illumina reads	G+C content (%)	No. of contigs	No. of illumina reads	Genome assembly N ₅₀ (bp)	No. of illumina reads	Genome assembly N ₅₀ (bp)	No. of protein-coding genes (5S, 16S, 23S)	complete rRNAs	size (bp)	No. of genome coverage (X)
KSC 339	<i>Staphylococcus saprophyticus</i>	2013-10	JAMAUC0000000000	SRX16346927	33.16	67	668,787	957,638	2,611	7,1,0	2,713,654	275		
KSC 351	<i>Priestia ayabhattai</i>	2013-10	JAMAUD0000000000	SRX16346928	38.01	129	1,818,110	944,494	5,491	13,0,1	5,394,993	375		
KSC 386	<i>Bacillus subtilis</i>	2013-10	JAMAUE0000000000	SRX16346929	45.48	846	1,510,313	1,048,650	5,014	8,1,0	4,623,969	362		
KSC 418	<i>Paenibacillus cellulostrophicus</i>	2013-10	JAMAUF0000000000	SRX16346930	53.16	47	1,881,832	4,455,811	6,501	8,0,0	7,260,279	284		
KSC 432	<i>Weizmannia ginsengihumi</i>	2013-10	JAMAUH0000000000	SRX16346931	36.29	212	1,172,830	90,727	3,518	11,0,0	3,778,211	343		
KSC 591	<i>Bacillus subtilis</i>	2013-10	JAMAUH0000000000	SRX16342414	44.64	381	860,329	502,380	4,295	4,0,1	4,187,511	229		
KSC 640	<i>Bacillus pumilus</i>	2013-10	JAMAUH0000000000	SRX16342415	41.44	147	2,196,861	277,292	3,730	4,1,1	3,690,879	657		
KSC 657	<i>Nitella circulans</i>	2013-10	JAMAUH0000000000	SRX16342452	35.56	79	2,442,071	338,051	4,663	10,1,0	5,008,815	541		
MER 10	<i>Bacillus safensis</i>	2003-04-09	JAMAUH0000000000	SRX16342463	41.71	53	1,164,678	941,139	3,638	5,0,1	3,646,425	354		
MER 100	<i>Nitella taxi</i>	2004-04-20	JAMAVH0000000000	SRX16342525	37.7	70	2,556,818	874,164	5,281	9,1,1	5,558,241	515		
MER 101	<i>Paenibacillus illinoiensis</i>	2004-04-20	JAMAVB0000000000	SRX16342536	47.35	91	2,268,682	1,002,168	5,789	9,0,0	6,488,901	394		
MER 107	<i>Neobacillus mesonae</i>	2004-04-20	JAMBOW0000000000	SRX16342499	44.31	93	2,412,451	889,947	5,466	8,0,0	5,956,811	450		
MER 108	<i>Terribacillus saccharophilus</i>	2004-04-20	JAMAVC0000000000	SRX16342510	42.52	54	987,784	675,549	3,665	8,0,1	3,639,914	305		
MER 110	<i>Priestia megeterium</i>	2004-04-20	JAMAVD0000000000	SRX16342545	37.84	121	1,668,830	1,289,863	5,772	13,1,0	5,687,929	328		
MER 112	<i>Bacillus altitudinis</i>	2004-04-20	JAMAVE0000000000	SRX16342556	41.37	79	855,101	535,620	3,738	5,0,1	3,705,254	255		
MER 116	<i>Bacillus cereus</i>	2004-04-20	JAMAVF0000000000	SRX16342416	35.13	65	1,895,614	847,946	5,308	11,1,0	5,433,442	372		
MER 118	<i>Bacillus cereus</i>	2004-04-20	JAMAVG5000000000	SRX16342427	34.72	114	1,943,681	430,491	5,875	12,1,0	6,085,090	357		
MER 128	<i>Priestia megeterium</i>	2004-05-28	JAMAVH0000000000	SRX16342438	37.79	156	1,508,285	938,338	5,866	13,0,0	5,783,390	292		
MER 13	<i>Priestia koreensis</i>	2004-04-09	JAMAUM0000000000	SRX16342476	39.99	88	1,451,686	279,082	4,785	11,0,0	4,785,760	339		
MER 131	<i>Paenibacillus laetus</i>	2004-05-28	JAMAVI0000000000	SRX16342487	51	57	1,605,299	4,447,477	6,290	4,0,0	7,140,748	249		
MER 132	<i>Bacillus cereus</i>	2004-05-26	JAMAVJ0000000000	SRX16342447	34.99	55	1,300,785	1,104,589	5,504	11,0,0	5,651,989	256		
MER 135A	<i>Bacillus safensis</i>	2004-05-26	JAMAWQ0000000000	SRX16342448	41.27	72	1,261,935	697,687	3,982	5,1,0	3,915,961	359		
MER 145	<i>Priestia ayabhattai</i>	2004-05-28	JAMBOQ0000000000	SRX16342449	37.63	132	1,341,366	1,075,173	5,539	13,0,0	5,481,448	272		
MER 153	<i>Priestia ayabhattai</i>	2004-05-28	JAMAVK0000000000	SRX16342450	37.66	126	1,514,592	992,532	5,650	13,1,0	5,632,345	301		
MER 156	<i>Bacillus subtilis</i>	2004-05-26	JAMAVL0000000000	SRX16342451	43.56	118	1,544,947	606,528	4,377	6,0,1	4,296,488	401		
MER 157	<i>Paenibacillus egii</i>	2004-06-15	JAMAVM0000000000	SRX16342453	52.88	334	2,640,790	237,149	7,374	10,1,0	8,123,320	359		
MER 161	<i>Bacillus licheniformis</i>	2004-06-15	JAMAVN0000000000	SRX16342454	46.07	55	974,474	2,240,388	4,314	7,0,0	4,282,357	245		
MER 165	<i>Bacillus licheniformis</i>	2004-06-15	JAMAVO0000000000	SRX16342455	46.03	29	1,157,486	2,240,383	4,292	7,1,0	4,271,713	293		
MER 166	<i>Bacillus velezensis</i>	2004-06-15	JAMAVP0000000000	SRX16342456	45.94	120	971,171	367,388	4,369	9,0,1	4,412,102	242		
MER 169	<i>Bacillus velezensis</i>	2004-06-15	JAMAVQ0000000000	SRX16342457	46.48	367	856,709	385,121	4,627	9,0,1	4,544,742	205		
MER 170	<i>Priestia megeterium</i>	2004-06-15	JAMAVR0000000000	SRX16342458	37.67	126	1,343,731	1,011,460	5,663	15,0,0	5,639,457	265		
MER 172A	<i>Streptomyces pseudogriseolus</i>	2004-06-28	JAMAVS0000000000	SRX16342459	72.43	132	536,706	166,114	6,596	5,1,0	7,637,093	73		
MER 180	<i>Paenibacillus</i> sp.	2004-06-28	JAMAVT0000000000	SRX16342460	46.52	129	2,045,322	344,519	5,798	7,0,0	6,744,104	339		
MER 189	<i>Staphylococcus capitis</i>	2004-06-28	JAMAVU0000000000	SRX16342461	32.81	72	747,197	673,926	2,293	7,1,0	2,449,216	339		
MER 193	<i>Exiguobacterium</i> sp.	2004-06-28	JAMAVV0000000000	SRX16342462	48.07	149	1,280,301	96,253	3,019	9,0,0	2,936,244	489		
MER 196A	<i>Streptomyces thermophilaceus</i>	2004-03-30	JAMAVW0000000000	SRX16342464	72.39	177	1,120,250	243,441	4,710	4,0,0	5,572,416	216		
MER 20	<i>Sporosarcina aquimarina</i>	2003-04-09	JAMBON0000000000	SRX16342516	41.63	38	969,673	474,897	3,308	8,1,0	3,423,265	311		(Continued on next page)

TABLE 1 (Continued)

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MER 26	<i>Paenibacillus polysaccharolyticus</i>	2003-04-09	JAMAUN0000000000	SRX16342517	45.8	95	1,876,503	390,937	5,511	8,0,0	6,431,905	323
MER 33	<i>Mesobacillus</i> sp.	2003-04-09	JAMAU0000000000	SRX16342518	42.95	83	1,784,978	377,099	4,616	8,0,0	4,787,833	414
MER 36	<i>Paenibacillus motobiensis</i>	2003-04-10	JAMAUP0000000000	SRX16342519	46.37	84	2,000,963	877,394	5,101	6,0,0	5,858,058	381
MER 37	<i>Paenibacillus pasadenensis</i>	2003-04-10	JAMBOT0000000000	SRX16342520	53	101	1,108,751	490,536	4,673	4,0,0	5,301,299	228
MER 46	<i>Metabacillus littoralis</i>	2003-04-09	JAMAUQ0000000000	SRX16342521	35.5	115	2,326,433	243,754	5,324	15,0,0	5,544,653	457
MER 47	<i>Sporosarcina luteola</i>	2003-04-09	JAMBOK0000000000	SRX16342522	44.89	31	541,805	2,093,321	3,191	7,0,1	3,306,674	182
MER 48	<i>Mesobacillus</i> sp.	2003-04-09	JAMAUV0000000000	SRX16342523	42.95	65	1,745,171	733,545	4,616	8,0,0	4,784,164	405
MER 50_2	<i>Paenibacillus macerans</i>	2003-04-09	JAMBOE0000000000	SRX16342524	52.02	137	2,502,116	363,305	6,312	4,0,0	7,289,640	322
MER 51	<i>Brevibacillus</i> sp.	2003-04-09	JAMAUS0000000000	SRX16342526	47.35	105	1,847,069	384,568	5,926	5,0,0	6,300,854	327
MER 53_1	<i>Neobacillus niaciini</i>	2003-04-09	JAMBOX0000000000	SRX16342527	42.32	132	2,759,808	249,238	5,533	13,0,0	5,696,635	543
MER 6	<i>Nitella</i> sp.	2003-04-09	JAMAUK0000000000	SRX16342528	38.07	157	1,281,869	160,136	5,457	9,1,1	5,627,590	254
MER 62	<i>Hydrogenophaga intermediata</i>	2003-03-05	JAMBNO0000000000	SRX16342529	66.86	150	1,197,190	189,322	4,435	2,2,2	4,651,607	281
MER 65	<i>Prestia megaterium</i>	2003-03-13	JAMAUT0000000000	SRX16342530	37.92	110	1,577,240	1,914,888	5,483	15,1,0	5,407,622	326
MER 73	<i>Peribacillus frigitorolens</i>	2003-03-13	JAMAUU0000000000	SRX16342531	40.26	154	1,521,411	261,737	5,391	9,0,0	5,714,701	293
MER 74	<i>Neobacillus</i> sp.	2003-03-11	JAMAUV0000000000	SRX16342532	38.82	147	1,010,466	241,461	5,230	19,0,0	5,541,816	204
MER 78	<i>Paenibacillus</i> sp.	2003-03-11	JAMAUW0000000000	SRX16342533	44.73	87	1,899,338	561,118	5,008	8,0,0	5,519,166	384
MER 82	<i>Cytobacillus horneckiae</i>	2003-04-17	JAMAUY0000000000	SRX16342534	37.8	90	1,253,825	715,509	5,041	9,1,0	5,219,193	270
MER 89	<i>Bacillus subtilis</i>	2003-04-03	JAMAUY0000000000	SRX16342535	43.71	75	669,189	323,094	4,014	5,1,0	4,049,231	185
MER 99_2	<i>Paenibacillus</i> sp.	2004-04-21	JAMAUZZ0000000000	SRX16342537	44.85	77	2,016,740	916,723	5,679	9,0,0	6,526,312	346
MER TA 106	<i>Cytobacillus oceanisediminis</i>	2013-07-30	JAMAAWE0000000000	SRX16342538	41.3	183	1,123,154	219,663	5,444	11,1,0	5,516,092	226
MER TA 107	<i>Neobacillus mesonae</i>	2013-08-09	JAMBNO0000000000	SRX16342539	38.75	182	2,115,476	110,087	5,086	15,0,0	5,410,113	434
MER TA 111	<i>Fictibacillus nathiensis</i>	2013-07-17	JAMBOD0000000000	SRX16342492	39.49	78	1,398,058	385,213	4,208	6,0,0	4,217,690	369
MER TA 112	<i>Streptococcus oralis</i>	2013-08-15	JAMAWF0000000000	SRX16342493	41.35	51	442,268	298,081	1,900	3,1,0	2,019,356	243
MER TA 114	<i>Cytobacillus kochii</i>	2013-08-01	JAMAWG0000000000	SRX16342494	36.67	83	2,220,982	759,874	4,544	9,0,0	4,661,354	527
MER TA 13	<i>Rummeliibacillus stabekii</i>	2013-06-27	JAMAVX0000000000	SRX16342495	37.41	68	1,020,678	953,447	3,251	12,0,1	3,349,733	340
MERTA 136-3-2	<i>Bacillus halotolerans</i>	2013-07-02	JAMAWH0000000000	SRX16342496	44.05	178	1,693,236	2,123,097	4,136	10,1,0	4,165,036	455
MERTA 137-5	<i>Bacillus subtilis</i>	2013-07-03	JAMAWI0000000000	SRX16342497	43.41	156	1,567,322	110,716	4,178	7,1,0	4,124,121	424
MERTA 138-1	<i>Alkalihalobacillus rhizosphaerae</i>	2013-06-27	JAMAWJ0000000000	SRX16342498	44.74	68	1,561,971	413,356	4,035	7,0,0	4,189,294	414
MERTA 138-2	<i>Cytobacillus oceanisediminis</i>	2013-07-17	JAMAWK0000000000	SRX16342500	41.04	133	1,892,273	153,567	5,559	9,0,0	5,681,886	373
MERTA 139-2	<i>Oceanobacillus profundus</i>	2013-07-18	JAMAWL0000000000	SRX16342501	37.64	90	803,015	262,861	4,334	8,0,0	4,561,942	197
MERTA 14	<i>Kocuria palustris</i>	2013-07-23	JAMAVY0000000000	SRX16342502	70.54	71	1,418,798	307,465	2,466	1,1,1	2,858,109	542
MERTA 152	<i>Mesobacillus maritimus</i>	2013-07-17	JAMBNR0000000000	SRX16342503	39.02	160	3,151,095	261,852	4,878	19,0,0	5,260,991	654
MERTA 17	<i>Psychrobacillus</i> sp.	2013-08-09	JAMAVZ0000000000	SRX16342504	44.91	121	1,923,583	343,608	4,245	7,0,0	4,324,992	496
MERTA 170	<i>Mesobacillus subterraneus</i>	2013-07-18	JAMBOT0000000000	SRX16342505	42.04	77	796,197	299,944	4,599	11,1,0	4,670,006	188

(Continued on next page)

TABLE 1 (Continued)

Strain name	Taxonomic identification	Date of isolation (yr/mo/day)	GenBank accession no.	SRA accession no. for illumina reads	G+C content (%)	No. of contigs	No. of illumina reads	Genome assembly N ₅₀ (bp)	No. of illumina reads	No. of protein-coding genes (5S, 16S, 23S)	Genome size (bp)	Genome coverage (×)
MER TA 171	<i>Psychrobacillus</i> sp. <i>Ureibacillus chungkukjangi</i>	2013-07-18 2013-07-17	JAMAWN000000000000 JAMAWO000000000000	SRX16342506 SRX16342507	37.17 36.18	114 172	1,399,241 829,210	146,555 109,322	3,976 4,264	9,1,0 11,1,0	4,064,209 4,459,889	381 208
MER TA 176												
MER TA 18	<i>Staphylococcus warneri</i>	2013-06-27	JAMAWA000000000000	SRX16342508	32.65	27	566,180	920,533	2,266	7,1,1	2,424,208	256
MER TA 181	<i>Metabacillus halosacharavorans</i>	2013-07-17	JAMAWP000000000000	SRX16342509	35.74	137	2,797,792	202,899	5,666	10,0,0	6,017,055	520
MERTA 32b	<i>Panococcus</i> sp.	2013-08-12	JAMCAN000000000000	SRX17618098	46.17	94	1,585,957	2,020,338	3,209	5,1,0	3,245,854	546
MERTA 38	<i>Penibacillus glycantilyticus</i>	2013-07-24	JAMBNF000000000000	SRX16342511	50.3	105	1,743,564	537,285	5,968	6,0,0	6,724,235	288
MERTA 48	<i>Sporosarcina luteola</i>	2013-07-23	JAMBNN000000000000	SRX16342512	44.5	47	1,529,788	2,309,686	3,444	8,0,0	3,552,921	482
MERTA 81-3	<i>Penibacillus</i> sp.	2013-07-23	JAMAWB000000000000	SRX16342513	48.69	173	1,832,882	307,130	5,899	8,0,0	6,872,147	296
MERTA 82	<i>Cyrtobacillus kochii</i>	2014-07-23	JAMAWC000000000000	SRX16342514	36.97	197	2,780,397	759,874	4,654	9,0,0	4,712,805	659
MERTA 86	<i>Metabacillus litoralis</i>	2013-07-30	JAMBNW000000000000	SRX16342515	36.5	211	2,110,902	227,801	5,337	15,0,0	5,990,291	390
MERTA 87	<i>Neobacillus niacini</i>	2013-07-30	JAMBBO000000000000	SRX16342540	38.14	111	2,406,523	495,822	5,107	13,0,0	5,316,554	504
MERTA 97	<i>Staphylococcus capitis</i>	2013-08-09	JAMAWD000000000000	SRX16342541	33.42	150	860,100	469,804	2,337	7,0,0	2,456,498	390
MER 9	<i>Sporosarcina luteola</i>	2003-04-09	JAMBNO000000000000	SRX16342542	44.52	92	871,704	443,563	3,551	7,0,0	3,602,600	272
MERTA 168	<i>Nitella</i> sp.	2013-07-18	JAMAWM000000000000	SRX16342543	35.05	199	1,450,973	100,872	4,786	10,0,0	5,178,238	306
MERTA 154	<i>Solibacillus isronensis</i>	2013-07-17	JAMBCC000000000000	SRX16342544	38.62	65	1,166,522	2,361,702	3,684	11,0,1	3,808,720	337
MPF 19	<i>Bacillus velezensis</i>	2004-05-01	JAMAW500000000000	SRX16342546	48.09	699	3,666,662	155,510	4,354	8,6,6	4,203,241	98
MPF 2	<i>Bacillus licheniformis</i>	2004-05-01	JAMAWY000000000000	SRX16342547	46.09	142	1,271,867	612,391	4,505	7,0,1	4,398,042	319
MPF 24	<i>Bacillus subtilis</i>	2004-05-06	JAMAWT000000000000	SRX16342548	43.86	168	1,310,983	1,057,136	4,260	7,0,0	4,199,270	349
MPF 38	<i>Bacillus paralicheniformis</i>	2004-05-06	JAMAWU000000000000	SRX16342549	45.91	55	1,027,464	1,116,529	4,287	7,0,0	4,395,789	259
MPF 57	<i>Bacillus intestinalis</i>	2004-05-19	JAMAWV000000000000	SRX16342550	44.03	115	1,404,213	325,227	3,975	9,0,0	4,032,203	383
MPF 67	<i>Bacillus licheniformis</i>	2004-05-11	JAMAWX000000000000	SRX16342551	45.97	82	1,062,046	583,595	4,430	7,0,1	4,369,009	268
MPF 76A	<i>Bacillus licheniformis</i>	2004-05-11	JAMAWX000000000000	SRX16342552	48.09	1093	2,123,917	491,455	5,461	7,0,1	4,892,212	484
MPF 8	<i>Bacillus licheniformis</i>	2004-05-01	JAMAWR000000000000	SRX16342553	46.54	400	1,453,562	553,893	4,732	7,0,1	4,521,756	359
MSL 004.1.2	<i>Rothia dentocariosa</i>	2008-03-17	JAMAWZ000000000000	SRX16342554	53.94	76	616,186	389,714	2,098	3,1,0,1	2,448,390	280
MSL 016.1	<i>Staphylococcus epidermidis</i>	2008-03-27	JAMAXA000000000000	SRX16342555	32.08	72	983,790	187,847	2,236	7,1,0	2,462,434	445
MSL 036.1	<i>Brevibacillus invocatus</i>	2008-05-14	JAMAXB000000000000	SRX16342557	48.69	214	1,135,485	93,236	4,810	5,0,0	4,940,093	258
MSL 047.1	<i>Sphingopyxis alaskensis</i>	2008-05-14	JAMAXC000000000000	SRX16342558	65.11	75	1,639,175	145,245	3,615	1,1,1	3,777,004	475
MSL 047.2	<i>Sphingomonas paucimobilis</i>	2008-05-14	JAMAXD000000000000	SRX16342559	65.48	71	2,658,702	593,513	4,195	1,1,1	4,553,552	644
MSL 058.1.2	<i>Metabacillus litoralis</i>	2008-07-21	JAMAXE000000000000	SRX16342560	35.6	122	2,116,836	349,633	5,388	15,0,0	5,577,721	417
MSL 060.1.1	<i>Bacillus atrophaeus</i>	2008-07-21	JAMAXF000000000000	SRX16342561	43.2	26	1,049,730	1,047,913	3,912	7,1,1	4,086,418	273
MSL 107	<i>Staphylococcus epidermidis</i>	2008-10-08	JAMAXG000000000000	SRX16342562	32.13	64	1,243,709	183,913	2,276	6,0,0	2,512,070	552
MSL 160.2	<i>Bacillus velezensis</i>	2008-11-12	JAMAXH000000000000	SRX16342563	46.43	79	1,304,922	382,423	3,776	7,0,0	4,006,624	364
MSL 172.1.2	<i>Bacillus safensis</i>	2008-12-02	JAMAXI000000000000	SRX16342465	41.67	32	585,827	946,465	3,680	4,0,0	3,671,895	177
MSL 173.2.2	<i>Peribacillus simplex</i>	2008-12-02	JAMAXK000000000000	SRX16342466	39.84	227	1,856,358	102,406	5,323	9,0,0	5,725,607	361
MSL 179.1	<i>Heyndrickxia oronina</i>	2008-12-04	JAMAXL000000000000	SRX16342467	34.83	120	2,771,284	152,837	5,134	11,0,0	5,286,683	579
MSL 185.1	<i>Caldibacillus thermoamylivorans</i>	2008-12-08	JAMAXM000000000000	SRX16342417	37.36	111	911,571	277,299	3,456	9,0,0	3,809,017	259
MSL 187.1	<i>Paenibacillus lactis</i>	2008-12-08	JAMAXN000000000000	SRX16342418	52.01	96	1,872,690	556,132	5,905	6,1,0	6,686,450	308

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TABLE 1 (Continued)

Strain name	Taxonomic identification	Date of isolation (yr/ mo/day)	GenBank accession no.	SRA accession no. for illumina reads	G+C content (%)	No. of contigs	No. of illumina reads	No. of illumina reads	Genome assembly N ₅₀ (bp)	No. of protein-coding genes (5S, 16S, 23S)	No. of complete rRNAs	No. of genome size (bp)	Genome coverage (X)
MSL 200.1	<i>Priestia megaterium</i>	2008-12-04	JAMAXV00000000000	SRX16342419	37.98	112	2,287,220	1,185,537	5,366	12,0,0	5,295,778	482	
MSL 225.1.2	<i>Dormibacillus indicus</i>	2009-01-15	JAMBOO00000000000	SRX16342420	43.49	181	1,271,139	161,986	4,858	23,0,0	5,083,418	278	
MSL 259.1	<i>Staphylococcus lugdunensis</i>	2008-04-06	JAMAXP00000000000	SRX16342421	35.88	455	737,693	302,134	2,803	5,0,0	2,789,329	297	
MSL 300.3	<i>Staphylococcus xylosus</i>	2014-07-23	JAMAXW00000000000	SRX16342422	32.7	78	732,430	291,655	2,679	7,1,1	2,864,935	285	
MSL 314.1	<i>Staphylococcus hominis</i>	2010-06-28	JAMAXQ00000000000	SRX16342423	31.51	70	882,042	362,212	2,130	6,0,0	2,202,842	445	
MSL 316.2	<i>Staphylococcus warneri</i>	2010-06-28	JAMAXR00000000000	SRX16342424	32.48	37	809,071	431,070	2,409	5,1,0	2,550,295	356	
MSL 321.1	<i>Micrococcus luteus</i>	2010-06-28	JAMAXS00000000000	SRX16342425	72.9	126	1,098,795	174,685	2,311	1,0,0	2,546,255	468	
MSL 336.2	<i>Ralstonia picketii</i>	2010-06-28	JAMAXT00000000000	SRX16342426	63.35	44	1,779,304	460,861	5,262	1,1,1	5,563,662	352	
MSL 348	<i>Cupriavidus pauculus</i>	2010-04-20	JAMAXU00000000000	SRX16342428	64.08	82	1,395,623	425,000	3,760	1,1,1	6,426,329	237	
MSL 359	<i>Kocuria rosea</i>	2010-05-06	JAMAXV00000000000	SRX16342429	72.48	129	959,164	265,844	3,612	1,1,0	3,983,493	259	
MSL 140.1	<i>Brevibacillus borstelensis</i>	2008-10-08	JAMAXH00000000000	SRX16342430	51.36	209	2,022,985	103,406	5,067	3,1,0	5,382,697	419	
ODYSSEY 48 V2	<i>Curtobacterium sp.</i>	2007-01-29	JAMAXX00000000000	SRX16342431	71.88	81	901,252	346,312	3,217	2,1,0	3,485,755	286	
P10	<i>Microbacterium</i> <i>alevorans</i>	2003-12	JAMBOV00000000000	SRX16342432	69.95	31	1,265,533	641,097	2,993	3,0,1	3,171,571	441	
P100	<i>Rothia</i> sp.	2003-12	JAMAYG00000000000	SRX16342433	56.18	20	646,400	515,480	2,107	3,1,1	2,404,879	297	
P106	<i>Alkalihalobacillus oceanii</i>	2003-12	JAMBOS00000000000	SRX16342434	46.36	146	2,330,371	138,530	4,178	8,0,1	4,381,113	589	
P107	<i>Priestia abyhattai</i>	2003-12	JAMAYH00000000000	SRX16342435	37.64	98	1,469,448	1,101,254	5,663	13,0,0	5,597,164	289	
P112	<i>Cellulosimicrobium funkei</i>	2003-12	JAMAYI00000000000	SRX16342436	74.71	65	721,097	514,644	3,743	1,1,1	4,266,893	176	
P121	<i>Priestia megaterium</i>	2003-12	JAMAYJ00000000000	SRX16342437	37.76	92	1,223,494	752,388	5,608	13,0,1	5,578,758	242	
P18	<i>Mesobacillus subterraneus</i>	2003-12	JAMBNN00000000000	SRX16342439	42.33	106	2,401,577	200,889	4,984	6,1,0	5,105,592	523	
P25	<i>Microbacterium endense</i>	2003-12	JAMAXY00000000000	SRX16342440	70.46	26	1,223,278	360,559	3,132	1,1,1	3,486,885	376	
P26	<i>Microbacterium</i> sp.	2003-12	JAMAXZ00000000000	SRX16342468	70.34	43	2,257,191	588,147	3,244	1,0,1	3,517,995	699	
P30	<i>Microbacterium hydrocarboxyloxydans</i>	2003-12	JAMBOY00000000000	SRX16342469	69.02	27	769,560	838,703	3,288	2,0,1	3,483,679	239	
P42	<i>Alkalihalophilus marmarensis</i>	2003-12	JAMAYA00000000000	SRX16342470	40	82	949,855	206,984	4,125	7,0,0	4,103,950	257	
P67	<i>Scutellifella horikoshii</i>	2003-12	JAMAYB00000000000	SRX16342471	41.05	68	1,547,227	410,581	4,695	9,0,0	4,708,311	368	
P7	<i>Georgenia satyanarayanae</i>	2003-12	JAMBNZ00000000000	SRX16342472	72.21	196	2,481,880	304,175	3,395	1,1,0	3,723,384	718	
P75	<i>Staphylococcus capitis</i>	2003-12	JAMAYC00000000000	SRX16342473	32.83	72	562,317	503,111	2,463	7,0,0	2,597,991	240	
P83	<i>Staphylococcus capitis</i>	2003-12	JAMAYD00000000000	SRX16342474	34.11	272	551,867	672,612	2,542	7,0,0	2,583,208	240	
P86	<i>Nocardiooides</i> sp.	2003-12	JAMAYE00000000000	SRX16342475	74.08	64	2,061,229	1,297,617	3,697	3,1,1	4,031,233	553	
P97	<i>Curtobacterium</i> sp.	2003-12	JAMAYF00000000000	SRX16342477	71.82	248	382,234	219,850	3,469	3,1,0	3,616,588	117	
PF24B.2	<i>Robertmurraya korlensis</i>	2007-08-20	JAMBNS00000000000	SRX16342478	38.22	191	1,836,561	290,106	4,733	13,0,0	4,761,956	428	
PF3F.2	<i>Priestia endophytica</i>	2007-08-20	JAMAYK00000000000	SRX16342479	36.58	51	1,159,426	3,768,234	5,003	9,0,0	5,145,492	248	
PF4F.2.1	<i>Cyrobacillus oceanisendiminius</i>	2007-08-20	JAMAYL00000000000	SRX16342480	41.45	94	2,220,633	703,746	5,136	10,1,0	5,254,108	470	
RA 14A.10	<i>Agronomycetes mediolanus</i>	2007-04-06	JAMBNX00000000000	SRX16342481	71.47	90	853,226	376,941	3,757	1,1,1	4,038,592	225	
TA 121-4	<i>Bacillus subtilis</i>	2004-03-08	JAMAYN00000000000	SRX16342482	73.04	103	733,140	195,078	2,335	1,1,0	2,559,014	306	
TA 127	<i>Micrococcus luteus</i>	2004-03-08	JAMAYO00000000000	SRX16342483	73.08	106	282,980	228,776	2,225	2,0,0	2,454,472	122	
TA 149	<i>Micrococcus luteus</i>	2004-03-30	JAMAYP00000000000	SRX16342484	44.57	137	1,361,878	202,381	4,315	7,0,1	4,492,163	339	
TA 170	<i>Alkalihalobacillus clausii</i>	2004-03-30	JAMAYQ00000000000	SRX16342485	42.07	118	2,852,326	299,670	4,599	11,1,0	4,682,835	682	

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TABLE 1 (Continued)

Strain name	Taxonomic identification	Date of isolation (yr/ mo/day)	GenBank accession no.	SRA accession no. for Illumina reads	G+C content (%)	No. of contigs	No. of Illumina reads	Genome assembly N ₅₀ (bp)	No. of protein-coding genes (5S, 16S, 23S)	No. of complete rRNAs	Genome size (bp)	Genome coverage (×)
TA 172	<i>Mesobacillus subterraneus</i>	2004-03-30	JAMBNT0000000000	SRX16342486	40.51	93	2,255,199	533,846	4,951	8,1,0	5,059,287	489
TA 28	<i>Metabacillus iatiensis</i>	2004-02-25	JAMAYR0000000000	SRX16342488	73.14	73	465,310	158,923	3,269	1,1,1	3,635,835	133
TA 29	<i>Kocuria rosea</i>	2012-07-30	JAMBOG0000000000	SRX16342489	42.96	112	2,081,125	265,106	4,374	5,0,0	4,885,757	464
TA 33-2	<i>Paenibacillus camelliae</i>	2013-07-23	JAMBNY0000000000	SRX16342490	35	53	694,264	526,229	2,340	4,1,1	2,516,602	303
TA 76	<i>Carnobacterium inhibens</i>	2004-02-17	JAMAYN0000000000	SRX16342491	38.92	203	2,196,655	209,477	5,964	16,0,0	6,523,156	374
TA 104	<i>Neobacillus cucumis</i>	2004-02-06	JAMBH0000000000	SRX16342441	43.83	78	1,210,078	473,068	4,003	5,0,1	4,048,329	328
TPS 10-6-1	<i>Brevibacillus borstelensis</i>	2006-08-24	JAMAYT0000000000	SRX16342442	51.39	257	1,013,852	81,183	5,155	2,0,0	5,437,219	207
TPS 11-9-1	<i>Caldibacillus thermoamylavorans</i>	2006-08-24	JAMAYU0000000000	SRX16342443	37.43	291	678,229	68,324	3,523	10,0,0	3,812,260	182
TPS 14-3-1	<i>Brevibacillus borstelensis</i>	2006-04-26	JAMAYV0000000000	SRX16342444	51.57	231	835,682	96,347	5,088	3,1,0	5,368,369	171
TPS 8-13-1	<i>Brevibacillus borstelensis</i>	2006-09-20	JAMAYS0000000000	SRX16342445	51.36	237	1,999,409	77,807	5,096	3,1,0	5,389,870	414
V41-32	<i>Janibacter melonis</i>	2013-02-26	JAMAYW0000000000	SRX16342446	72.4	98	783,955	415,084	3,439	1,0,0	3,628,094	231

^aThe taxonomic identification was based off the species identification of GTDB-Tk, with adjustments made during submission to NCBI. The number of complete rRNAs does not take into account that all strains contain partial 16S rRNA.

45 s. Library preparation and quantification of DNA were executed on a Microlab STAR automated liquid handling system (Hamilton Bonaduz AG, Switzerland). The pooled libraries were then quantified using the KAPA library quantification kit for Illumina (Kapa Biosystems, USA). The libraries were sequenced using the Illumina HiSeq platform, with a 250-bp paired-end protocol. Adapters were trimmed from the raw reads using Trimmomatic 0.30, with a sliding cutoff of Q15 (3). SPAdes 2.7 (4) was used to perform *de novo* assembly of the samples, and the contigs were annotated using Prokka 1.11 (5). The assembled sequences were queried against the SILVA LTP 16S rRNA gene type strain database. Sequences with >98.7% sequence similarity to SILVA reference sequence were assigned a species level taxonomic identification. This screening process down-selected 191 isolates, which were sent for whole-genome sequencing (WGS). All 191 isolates had 16S sequences with greater than 98.7% similarity to a SILVA reference sequence. For whole-genome sequencing, DNA was also sent to MicrobesNG for library preparation and sequencing. All library preparation, sequencing, read trimming, quality control, and assembly were performed using the same procedures as described for 16S sequencing. The read quality was assessed using in-house scripts in combination with the following software: SAMtools (6), BEDTools (7), and BWA-MEM (8). The assembly quality was assessed using QUAST (9), and CheckM (10) was used to assess the read quality. All 191 sequences were >90% complete, with <5% contamination. The Genome Taxonomy Database Toolkit (GTDB-Tk) (11) was used to provide the final species level identification that was used for isolate identification. No new genus or species designations were assigned to any of the strains.

The assembled draft genomes were submitted for annotation using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP). The assembly statistics for all 191 strains are provided in Table 1.

Data availability. The 16S rRNA sequences, whole-genome sequences, and Sequence Read Archive (SRA) submission data were submitted to the National Center for Biotechnology Information (NCBI) under the BioProject accession number [PRJNA832800](#) and SRA accession number [SRP387068](#). The draft genome sequences of all 191 isolates have been deposited at NCBI under the accession numbers provided in Table 1.

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REFERENCES

1. National Aeronautics and Space Administration. 2010. Handbook for the microbial examination of space hardware. NASA-HDBK-6022. National Aeronautics and Space Administration, Washington, DC. https://explorers.larc.nasa.gov/2019APSMEX/SMEX/pdf_files/NASA-HDBK-6022b.pdf.
2. Seuylemezian A, Aronson HS, Tan J, Lin M, Schubert W, Vaishampayan P. 2018. Development of a custom MALDI-TOF MS database for species-level identification of bacterial isolates collected from spacecraft and associated surfaces. *Front Microbiol* 9:780. <https://doi.org/10.3389/fmicb.2018.00780>.
3. Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* 30:2114–2120. <https://doi.org/10.1093/bioinformatics/btu170>.
4. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotnik AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>.
5. Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. *Bioinformatics* 30:2068–2069. <https://doi.org/10.1093/bioinformatics/btu153>.
6. Danecek P, Bonfield JK, Liddle J, Marshall J, Ohan V, Pollard MO, Whitwham A, Keane T, McCarthy SA, Davies RM, Li H. 2021. Twelve years of SAMtools and BCFtools. *Gigascience* 10:giab008. <https://doi.org/10.1093/gigascience/giab008>.
7. Quinlan AR, Ira MH. 2010. BEDTools: a flexible suite of utilities for comparing genomic features. *Bioinformatics* 26:841–842. <https://doi.org/10.1093/bioinformatics/btq033>.
8. Li H. 2013. Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM. *arXiv* 1303.3997v2 [q-bio.GN]. <https://doi.org/10.48550/arXiv.1303.3997>.
9. Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUAST: quality assessment tool for genome assemblies. *Bioinformatics* 29:1072–1075. <https://doi.org/10.1093/bioinformatics/btt086>.
10. Parks DH, Imelfort M, Skennerton CT, Hugenholtz P, Tyson GW. 2015. CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. *Genome Res* 25:1043–1055. <https://doi.org/10.1101/gr.186072.114>.
11. Chaumeil PA, Mussig AJ, Hugenholtz P, Parks DH. 2019. GTDB-Tk: a toolkit to classify genomes with the Genome Taxonomy Database. *Bioinformatics* 36:1925–1927. <https://doi.org/10.1093/bioinformatics/btz848>.